

seqlist.txt

SEQUENCE LISTING

<110> Novartis AG
Wolfgang, Curt

<120> BIOMARKERS FOR THE PREDICTION OF
DRUG-INDUCED DIARRHOEA

<130> ON/4-33391A

<150> 60/508,973

<151> 2003-10-06

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2187

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (104)...(1618)

<223> Human interferon regulatory factor 5 (IRF5) mRNA
coding region

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ctggcgcagc cacgcaggcg caccgcagac agaccctct gcc atg aac cag tcc 115
Met Asn Gln Ser
1

atc cca gtg gct ccc acc cca ccc cgc cgc gtg cgg ctg aag ccc tgg 163
Ile Pro Val Ala Pro Thr Pro Pro Arg Arg Val Arg Leu Lys Pro Trp
5 10 15 20

ctg gtg gcc cag gtg aac agc tgc cag tac cca ggg ctt caa tgg gtc 211
Leu Val Ala Gln Val Asn Ser Cys Gln Tyr Pro Gly Leu Gln Trp Val
25 30 35

aac ggg gaa aag aaa tta ttc tgc atc ccc tgg agg cat gcc aca agg 259
Asn Gly Glu Lys Lys Leu Phe Cys Ile Pro Trp Arg His Ala Thr Arg
40 45 50

cat ggt ccc agc cag gac gga gat aac acc atc ttc aag gcc tgg gcc 307
His Gly Pro Ser Gln Asp Gly Asp Asn Thr Ile Phe Lys Ala Trp Ala
55 60 65

aag gag aca ggg aaa tac acc gaa ggc gtg gat gaa gcc gat ccg gcc 355
Lys Glu Thr Gly Lys Tyr Thr Glu Gly Val Asp Glu Ala Asp Pro Ala
70 75 80

aag tgg aag gcc aac ctg cgc tgt gcc ctt aac aag agc cgg gac ttc 403
Lys Trp Lys Ala Asn Leu Arg Cys Ala Leu Asn Lys Ser Arg Asp Phe
85 90 95 100

cgc ctc atc tac gac ggg ccc cgg gac atg cca cct cag ccc tac aag 451
Arg Leu Ile Tyr Asp Gly Pro Arg Asp Met Pro Pro Gln Pro Tyr Lys
105 110 115

atc tac gag gtc tgc tcc aat ggc cct gct ccc aca gac tcc cag ccc 499
Ile Tyr Glu Val Cys Ser Asn Gly Pro Ala Pro Thr Asp Ser Gln Pro
120 125 130

seq1ist.txt																
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Pro	Glu	Asp	Tyr	Ser	Phe	Gly	Ala	Gly	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
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gag	ctg	cag	agg	atg	ttg	cca	agc	ctg	agc	ctc	aca	gat	gca	gtg	cag	595
Glu	Leu	Gln	Arg	Met	Leu	Pro	Ser	Leu	Ser	Leu	Thr	Asp	Ala	Val	Gln	
	150					155					160					
tct	ggc	ccc	cac	atg	aca	ccc	tat	tct	tta	ctc	aaa	gag	gat	gtc	aag	643
Ser	Gly	Pro	His	Met	Thr	Pro	Tyr	Ser	Leu	Leu	Lys	Glu	Asp	Val	Lys	
165					170					175					180	
tgg	ccg	ccc	act	ctg	cag	ccg	ccc	act	ctg	cag	ccg	ccc	gtg	gtg	ctg	691
Trp	Pro	Pro	Thr	Leu	Gln	Pro	Pro	Thr	Leu	Gln	Pro	Pro	Val	Val	Leu	
				185					190					195		
ggt	ccc	cct	gct	cca	gac	ccc	agc	ccc	ctg	gct	cct	ccc	cct	ggc	aac	739
Gly	Pro	Pro	Ala	Pro	Asp	Pro	Ser	Pro	Leu	Ala	Pro	Pro	Pro	Gly	Asn	
			200					205					210			
cct	gct	ggc	ttc	agg	gag	ctt	ctc	tct	gag	gtc	ctg	gag	cct	ggg	ccc	787
Pro	Ala	Gly	Phe	Arg	Glu	Leu	Leu	Ser	Glu	Val	Leu	Glu	Pro	Gly	Pro	
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ctg	cct	gcc	agc	ctg	ccc	cct	gca	ggc	gaa	cag	ctc	ctg	cca	gac	ctg	835
Leu	Pro	Ala	Ser	Leu	Pro	Pro	Ala	Gly	Glu	Gln	Leu	Leu	Pro	Asp	Leu	
	230					235					240					
ctg	atc	agc	ccc	cac	atg	ctg	cct	ctg	acc	gac	ctg	gag	atc	aag	ttt	883
Leu	Ile	Ser	Pro	His	Met	Leu	Pro	Leu	Thr	Asp	Leu	Glu	Ile	Lys	Phe	
245					250					255					260	
cag	tac	cgg	ggg	cgg	cca	ccc	cgg	gcc	ctc	acc	atc	agc	aac	ccc	cat	931
Gln	Tyr	Arg	Gly	Arg	Pro	Pro	Arg	Ala	Leu	Thr	Ile	Ser	Asn	Pro	His	
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ggc	tgc	cgg	ctc	ttc	tac	agc	cag	ctg	gag	gcc	acc	cag	gag	cag	gtg	979
Gly	Cys	Arg	Leu	Phe	Tyr	Ser	Gln	Leu	Glu	Ala	Thr	Gln	Glu	Gln	Val	
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gaa	ctc	ttc	ggc	ccc	ata	agc	ctg	gag	caa	gtg	cgc	ttc	ccc	agc	cct	1027
Glu	Leu	Phe	Gly	Pro	Ile	Ser	Leu	Glu	Gln	Val	Arg	Phe	Pro	Ser	Pro	
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gag	gac	atc	ccc	agt	gac	aag	cag	cgc	ttc	tac	acg	aac	cag	ctg	ctg	1075
Glu	Asp	Ile	Pro	Ser	Asp	Lys	Gln	Arg	Phe	Tyr	Thr	Asn	Gln	Leu	Leu	
	310					315					320					
gat	gtc	ctg	gac	cgc	ggg	ctc	atc	ctc	cag	cta	cag	ggc	cag	gac	ctt	1123
Asp	Val	Leu	Asp	Arg	Gly	Leu	Ile	Leu	Gln	Leu	Gln	Gly	Gln	Asp	Leu	
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tat	gcc	atc	cgc	ctg	tgt	cag	tgc	aag	gtg	ttc	tgg	agc	ggg	cct	tgt	1171
Tyr	Ala	Ile	Arg	Leu	Cys	Gln	Cys	Lys	Val	Phe	Trp	Ser	Gly	Pro	Cys	
				345					350					355		
gcc	tca	gcc	cat	gac	tca	tgc	ccc	aac	ccc	atc	cag	cgg	gag	gtc	aag	1219
Ala	Ser	Ala	His	Asp	Ser	Cys	Pro	Asn	Pro	Ile	Gln	Arg	Glu	Val	Lys	
			360					365					370			
acc	aag	ctt	ttc	agc	ctg	gag	cat	ttt	ctc	aat	gag	ctc	atc	ctg	ttc	1267
Thr	Lys	Leu	Phe	Ser	Leu	Glu	His	Phe	Leu	Asn	Glu	Leu	Ile	Leu	Phe	
		375					380					385				
caa	aag	ggc	cag	acc	aac	acc	cca	cca	ccc	ttc	gag	atc	ttc	ttc	tgc	1315
Gln	Lys	Gly	Gln	Thr	Asn	Thr	Pro	Pro	Pro	Phe	Glu	Ile	Phe	Phe	Cys	
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seq1ist.txt

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Phe Gly Glu Glu Trp Pro Asp Arg Lys Pro Arg Glu Lys Lys Leu Ile
405 410 415 420

act gta cag gtg gtg cct gta gca gct cga ctg ctg ctg gag atg ttc 1411
Thr Val Gln Val Val Pro Val Ala Ala Arg Leu Leu Leu Glu Met Phe
425 430 435

tca ggg gag cta tct tgg tca gct gat agt atc cgg cta cag atc tca 1459
Ser Gly Glu Leu Ser Trp Ser Ala Asp Ser Ile Arg Leu Gln Ile Ser
440 445 450

aac cca gac ctc aaa gac cgc atg gtg gag caa ttc aag gag ctc cat 1507
Asn Pro Asp Leu Lys Asp Arg Met Val Glu Gln Phe Lys Glu Leu His
455 460 465

cac atc tgg cag tcc cag cag cgg ttg cag cct gtg gcc cag gcc cct 1555
His Ile Trp Gln Ser Gln Gln Arg Leu Gln Pro Val Ala Gln Ala Pro
470 475 480

cct gga gca ggc ctt ggt gtt ggc cag ggg ccc tgg cct atg cac cca 1603
Pro Gly Ala Gly Leu Gly Val Gly Gln Gly Pro Trp Pro Met His Pro
485 490 495 500

gct ggc atg caa taa caaggctgca gacggtgact ggccctggct tcctgggtgg 1658
Ala Gly Met Gln *

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cgggtgaggac tgatgtggag atgtgacagc cccgatgagc acctggctgg ctgcaggggc 1718
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cccctgcctt cccgggcctt tctctcctgg gctgtctctg gtctggctcag cctggctctc 1838
gggaaattca gccatgagca gggaaagaac tctcccaacc ctggggccta gctgtatagg 1898
aggaattgct taagggtggc ccactcttgt gattgcccc tttcctctgg caacaaaagc 1958
cagagtgttg tgggccaagt ccccccacag ggcccttgca gggcatggcc ctgatttccc 2018
tggtttgaga ctacttcct catctccctg tcctctgaga taatatgagt gagcacttag 2078
gtatcataatc agatgctcaa ggctggcagc taccctcttc ttgagagtcc aagaacctgg 2138
agcagaaata atttttatgt atttttgat taataaatgt taaaaacag 2187

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<210> 2
 <211> 1462
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (200)...(910)
 <223> Human cell division cycle 34 (CDC34) mRNA coding region

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<400> 2
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cggcgggcgg gcagaggagg aggcaggcgg cggccccggg ggctcccccc cggacgggtg 120
gcggccccgg ccgtctcgcg aactcgcggt ggtcgcgcg ccccgcgctg ctccgacccc 180
gggccccctc gccgcccgc atg gct cgg ccg cta gtg ccc agc tcg cag aag 232
Met Ala Arg Pro Leu Val Pro Ser Ser Gln Lys
1 5 10

```

```

gcg ctg ctg ctg gag ctc aag ggg ctg cag gaa gag ccg gtc gag gga 280
Ala Leu Leu Leu Glu Leu Lys Gly Leu Gln Glu Glu Pro Val Glu Gly
15 20 25

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```

ttc cgc gtg aca ctg gtg gac gag ggc gat cta tac aac tgg gag gtg 328
Phe Arg Val Thr Leu Val Asp Glu Gly Asp Leu Tyr Asn Trp Glu Val
30 35 40

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```

gcc atc ttc ggg ccc ccc aac acc tac tac gag ggc ggc tac ttc aag 376
Ala Ile Phe Gly Pro Pro Asn Thr Tyr Tyr Glu Gly Gly Tyr Phe Lys
45 50 55

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seq1ist.txt

```

gcg cgc ctc aag ttc ccc atc gac tac cca tac tct cca cca gcc ttt 424
Ala Arg Leu Lys Phe Pro Ile Asp Tyr Pro Tyr Ser Pro Pro Ala Phe
60 65 70 75

cgg ttc ctg acc aag atg tgg cac cct aac atc tac gag acg ggg gac 472
Arg Phe Leu Thr Lys Met Trp His Pro Asn Ile Tyr Glu Thr Gly Asp
80 85 90

gtg tgt atc tcc atc ctc cac ccg ccg gtg gac gac ccc cag agc ggg 520
Val Cys Ile Ser Ile Leu His Pro Pro Val Asp Asp Pro Gln Ser Gly
95 100 105

gag ctg ccc tca gag agg tgg aac ccc acg cag aac gtc agg acc att 568
Glu Leu Pro Ser Glu Arg Trp Asn Pro Thr Gln Asn Val Arg Thr Ile
110 115 120

ctc ctg agt gtg atc tcc ctc ctg aac gag ccc aac acc ttc tcg ccc 616
Leu Leu Ser Val Ile Ser Leu Leu Asn Glu Pro Asn Thr Phe Ser Pro
125 130 135

gca aac gtg gac gcc tcc gtg atg tac agg aag tgg aaa gag agc aag 664
Ala Asn Val Asp Ala Ser Val Met Tyr Arg Lys Trp Lys Glu Ser Lys
140 145 150 155

ggg aag gat cgg gag tac aca gac atc atc cgg aag cag gtc ctg ggg 712
Gly Lys Asp Arg Glu Tyr Thr Asp Ile Ile Arg Lys Gln Val Leu Gly
160 165 170

acc aag gtg gac gcg gag cgt gac ggc gtg aag gtg ccc acc acg ctg 760
Thr Lys Val Asp Ala Glu Arg Asp Gly Val Lys Val Pro Thr Thr Leu
175 180 185

gcc gag tac tgc gtg aag acc aag gcg ccg gcg ccc gag gag ggc tca 808
Ala Glu Tyr Cys Val Lys Thr Lys Ala Pro Ala Pro Asp Glu Gly Ser
190 195 200

gac ctc ttc tac gac gac tac tac gag gac ggc gag gtg gag gag gag 856
Asp Leu Phe Tyr Asp Asp Tyr Tyr Glu Asp Gly Glu Val Glu Glu Glu
205 210 215

gcc gac agc tgc ttc ggg gac gat gag gat gac tct ggc acg gag gag 904
Ala Asp Ser Cys Phe Gly Asp Asp Glu Asp Asp Ser Gly Thr Glu Glu
220 225 230 235

tcc tga caccaccaga ataaacttgc cgagtttacc tcactagggc cggacccgtg 960
Ser *

```

```

gctccttaga cgacagacta cctcacggag gttttgtgct ggtccccgtc tcctctgggt 1020
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aagagggggt gcccaccgc cactcacgtc actcggggct cgggtggacgg gcccagggtg 1140
ggagcggccg gcccacctgt cccctcgga ggggagctga gcccgacttc taccggggtc 1200
ccccagcttc cggactggcc gcaccccgga ggagccacgg gggcgctgct gggaacgtgg 1260
gcggggggcc gtttcctgac actaccagcc tgggaggccc aggtgtagcg gtccgagggg 1320
cccggtcctg cctgtcagct ccaggtcctg gagccacgtc cagcacagag tggacggatt 1380
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tgagaaaaaa aaaaaaaaaa aa 1462

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<210> 3
 <211> 3505
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (125)...(784)
 <223> Human BCL2/adenovirus E1B 19kDa interacting

seq1ist.txt
protein 3-like (BNIP3L) mRNA coding region

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tgtgttgctg cctgagtgcc ggagacggtc ctgctgctgc cgcagtcctg ccagctgtcc 120
gaca atg tcg tcc cac cta gtc gag ccg ccg ccg ccc ctg cac aac aac 169
Met Ser Ser His Leu Val Glu Pro Pro Pro Pro Leu His Asn Asn
1 5 10 15

aac aac aac tgc gag gaa aat gag cag tct ctg ccc ccg ccg gcc ggc 217
Asn Asn Asn Cys Glu Glu Asn Glu Gln Ser Leu Pro Pro Pro Ala Gly
20 25 30

ctc aac agt tcc tgg gtg gag cta ccc atg aac agc agc aat ggc aat 265
Leu Asn Ser Ser Trp Val Glu Leu Pro Met Asn Ser Ser Asn Gly Asn
35 40 45

gat aat ggc aat ggg aaa aat ggg ggg ctg gaa cac gta cca tcc tca 313
Asp Asn Gly Asn Gly Lys Asn Gly Gly Leu Glu His Val Pro Ser Ser
50 55 60

tcc tcc atc cac aat gga gac atg gag aag att ctt ttg gat gca caa 361
Ser Ser Ile His Asn Gly Asp Met Glu Lys Ile Leu Leu Asp Ala Gln
65 70 75

cat gaa tca gga cag agt agt tcc aga ggc agt tct cac tgt gac agc 409
His Glu Ser Gly Gln Ser Ser Ser Arg Gly Ser Ser His Cys Asp Ser
80 85 90 95

cct tcg cca caa gaa gat ggg cag atc atg ttt gat gtg gaa atg cac 457
Pro Ser Pro Gln Glu Asp Gly Gln Ile Met Phe Asp Val Glu Met His
100 105 110

acc agc agg gac cat agc tct cag tca gaa gaa gaa gtt gta gaa gga 505
Thr Ser Arg Asp His Ser Ser Gln Ser Glu Glu Glu Val Val Glu Gly
115 120 125

gag aag gaa gtc gag gct ttg aag aaa agt gcg gac tgg gta tca gac 553
Glu Lys Glu Val Glu Ala Leu Lys Lys Ser Ala Asp Trp Val Ser Asp
130 135 140

tgg tcc agt aga ccc gaa aac att cca ccc aag gag ttc cac ttc aga 601
Trp Ser Ser Arg Pro Glu Asn Ile Pro Pro Lys Glu Phe His Phe Arg
145 150 155

cac cct aaa cgt tct gtg tct tta agc atg agg aaa agt gga gcc atg 649
His Pro Lys Arg Ser Val Ser Leu Ser Met Arg Lys Ser Gly Ala Met
160 165 170 175

aag aaa ggg ggt att ttc tcc gca gaa ttt ctg aag gtg ttc att cca 697
Lys Lys Gly Gly Ile Phe Ser Ala Glu Phe Leu Lys Val Phe Ile Pro
180 185 190

tct ctc ttc ctt tct cat gtt ttg gct ttg ggg cta ggc atc tat att 745
Ser Leu Phe Leu Ser His Val Leu Ala Leu Gly Leu Gly Ile Tyr Ile
195 200 205

gga aag cga ctg agc aca ccc tct gcc agc acc tac tga gggaaaggaa 794
Gly Lys Arg Leu Ser Thr Pro Ser Ala Ser Thr Tyr *
210 215

aagcccctgg aaatgcgtgt gacctgtgaa gtgggtgtatt gtcacagtag cttattttgaa 854
cttgagacca ttgtaagcat gacccaacct accaccctgt ttttacatat ccaattccag 914
taactctcaa attcaatatt ttattcaaac tctgtttgagg cattttacta accttatacc 974
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seqlist.txt

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agccaaagtg attatgcatt cttcatctat ttttagttagc actttgtatc gttatataca 3434
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aactttaaaa a 3505

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<210> 4
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 <213> Homo sapiens

<220>
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 <222> (1)...(1314)

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1 5 10 15

atc agt gat gaa cat ggc atc gac ccc acc gcc acc tac cac ggg gac 96
Ile Ser Asp Glu His Gly Ile Asp Pro Thr Gly Thr Tyr His Gly Asp
20 25 30

agc gac ctg cag ctg gac cgc atc tct gtg tac tac aat gaa gcc aca 144
Ser Asp Leu Gln Leu Asp Arg Ile Ser Val Tyr Tyr Asn Glu Ala Thr
35 40 45

ggt ggc aaa tat gtt cct cgt gcc atc ctg gtg gat cta gaa cct ggg 192
Gly Gly Lys Tyr Val Pro Arg Ala Ile Leu Val Asp Leu Glu Pro Gly
50 55 60

acc atg gac tct gtt cgc tca ggt cct ttt gcc cag atc ttt aga cca 240
Thr Met Asp Ser Val Arg Ser Gly Pro Phe Gly Gln Ile Phe Arg Pro

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65			70					seq1ist.txt 75					80			
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ggc Gly	cac His	tac Tyr	aca Thr 100	gag Glu	ggc Gly	gcc Ala	gag Glu	ctg Leu 105	gtt Val	gat Asp	tct Ser	gtc Val	ctg Leu 110	gat Asp	gtg Val	336
gta Val	cgg Arg	aag Lys 115	gag Glu	gca Ala	gag Glu	agc Ser	tgt Cys 120	gac Asp	tgc Cys	ctg Leu	cag Gln	ggc Gly 125	ttc Phe	cag Gln	ctg Leu	384
acc Thr	cac His 130	tca Ser	ctg Leu	ggc Gly	ggg Gly	ggc Gly 135	aca Thr	ggc Gly	tct Ser	gga Gly	atg Met 140	ggc Gly	act Thr	ctc Leu	ctt Leu	432
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agt Ser	gtg Val	gtg Val	cct Pro	tca Ser 165	ccc Pro	aaa Lys	gtg Val	tct Ser	gac Asp 170	acc Thr	gtg Val	gtc Val	gag Glu	ccc Pro 175	tac Tyr	528
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tgg Trp	atc Ile	ccc Pro	aac Asn	aat Asn	gtc Val	aag Lys	aca Thr	gcc Ala	gtc Val	tgt Cys	gac Asp	atc Ile	cca Pro	cct Pro	cgt Arg	1056

seq1ist.txt

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1200			400
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			Met Ser 1
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gag aac cgt ttt tgt agc tgg gtg gat cag aaa ctc aac agc gaa gga Glu Asn Arg Phe Cys Ser Trp Val Asp Gln Lys Leu Asn Ser Glu Gly	20	25	30
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260			50
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308			
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seq1ist.txt

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Trp Arg Arg Ser Tyr Asn Val Thr Pro Pro Pro Ile Glu Glu Ser His			
115	120	125	130
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Pro Tyr Tyr Gln Glu Ile Tyr Asn Asp Arg Arg Tyr Lys Val Cys Asp			
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Val Pro Leu Asp Gln Leu Pro Arg Ser Glu Ser Leu Lys Asp Val Leu			
	150	155	160
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Glu Arg Leu Leu Pro Tyr Trp Asn Glu Arg Ile Ala Pro Glu Val Leu			
	165	170	175
cgtggc aaa acc att ctg ata tct gct cat gga aat agc agt agg gca			692
Arg Gly Lys Thr Ile Leu Ile Ser Ala His Gly Asn Ser Ser Arg Ala			
	180	185	190
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Leu Leu Lys His Leu Glu Gly Ile Ser Asp Glu Asp Ile Ile Asn Ile			
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Thr Leu Pro Thr Gly Val Pro Ile Leu Leu Glu Leu Asp Glu Asn Leu			
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Arg Ala Val Gly Pro His Gln Phe Leu Gly Asp Gln Glu Ala Ile Gln			
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gca gcc att aag aaa gta gaa gat caa gga aaa gtg aaa caa gct aaa			884
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Lys *			
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seqlist.txt

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Thr Ser 20 Leu Leu Gly Lys Val 25 Val Lys Thr His Gln 30 Phe Leu Phe Gly

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Ile Gly Arg Cys Pro Ile 40 Leu Ala Thr Gln 45 Pro Asn Cys Ser Gln 50

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Lys Ile Val 85 Gln Lys Ala Ala Pro 90 Glu Val Gln Glu Asp Val Lys Ala 95

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Phe Lys 100 Thr Asp Leu Pro Ser 105 Ser Val Ser Val 110 Ser Leu Arg Lys 110

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Phe	Val 260	Ala	Asn	Asp	Ser	Thr 265	Leu	Phe	Thr	Leu	Ala 270	Lys	Ile	Leu	Pro	
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seq1ist.txt

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seq1list.txt																
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cag Gln	gtg Val	ccc Pro 295	ccc Pro	aag Lys	aaa Lys	gtg Val	aag Lys	ggc Gly 300	tgg Trp	ctg Leu	ctg Leu	ccc Pro	gaa Glu 305	atg Met	cca Pro	968
ggc Gly	ctg Leu	atc Ile 310	acc Thr	gac Asp	atc Ile	ctg Leu	ctc Leu 315	tcc Ser	ctg Leu	gac Asp	gac Asp	cgc Arg 320	ttc Phe	ctc Leu	tac Tyr	1016
ttc Phe	agc Ser 325	aac Asn	tgg Trp	ctg Leu	cat His	ggg Gly 330	gac Asp	ctg Leu	agg Arg	cag Gln	tat Tyr 335	gac Asp	atc Ile	tct Ser	gac Asp	1064
cca Pro 340	cag Gln	aga Arg	ccc Pro	cgc Arg	ctc Leu 345	aca Thr	gga Gly	cag Gln	ctc Leu	ttc Phe 350	ctc Leu	gga Gly	ggc Gly	agc Ser	att Ile 355	1112
gtt Val	aag Lys	gga Gly	ggc Gly	cct Pro 360	gtg Val	caa Gln	gtg Val	ctg Leu	gag Glu 365	gac Asp	gag Glu	gaa Glu	cta Leu	aag Lys 370	tcc Ser	1160
cag Gln	cca Pro	gag Glu	ccc Pro 375	cta Leu	gtg Val	gtc Val	aag Lys	gga Gly 380	aaa Lys	cgg Arg	gtg Val	gct Ala	gga Gly 385	ggc Gly	cct Pro	1208
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seqlist.txt

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Ser Leu Tyr Ser Ala Trp Asp Lys Gln Phe Tyr Pro Asp Leu Ile Arg
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gaa ggc tct gtg atg ctg cag gtt gat gta gac aca gta aaa gga ggg 1352
Glu Gly Ser Val Met Leu Gln Val Asp Val Asp Thr Val Lys Gly Gly
      420      425      430      435

ctg aag ttg aac ccc aac ttc ctg gtg gac ttc ggg aag gag ccc ctt 1400
Leu Lys Leu Asn Pro Asn Phe Leu Val Asp Phe Gly Lys Glu Pro Leu
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Gly Pro Ala Leu Ala His Glu Leu Arg Tyr Pro Gly Gly Asp Cys Ser
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Ser Asp Ile Trp Ile *

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tactgaccac tgttgcttgt tgctcactgt gctgcttttc catgagctct tggaggcacc 1676
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      Diego blood group) (SLC4A1) mRNA coding region

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                               Met
                               1

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Glu Glu Leu Gln Asp Asp Tyr Glu Asp Met Met Glu Glu Asn Leu Glu
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cag gag gaa tat gaa gac cca gac atc ccc gag tcc cag atg gag gag 213
Gln Glu Glu Tyr Glu Asp Pro Asp Ile Pro Glu Ser Gln Met Glu Glu
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ccg gca gct cac gac acc gag gca aca gcc aca gac tac cac acc aca 261
Pro Ala Ala His Asp Thr Glu Ala Thr Ala Thr Asp Tyr His Thr Thr
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tca cac ccg ggt acc cac aag gtc tat gtg gag ctg cag gag ctg gtg 309
Ser His Pro Gly Thr His Lys Val Tyr Val Glu Leu Gln Glu Leu Val
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atg gac gaa aag aac cag gag ctg aga tgg atg gag gcg gcg cgc tgg 357
Met Asp Glu Lys Asn Gln Glu Leu Arg Trp Met Glu Ala Ala Arg Trp
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Val Gln Leu Glu Glu Asn Leu Gly Glu Asn Gly Ala Trp Gly Arg Pro

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ttc Phe	acc Thr 115	aag Lys	ggt Gly	act Thr	gtt Val	ctc Leu 120	cta Leu	gac Asp	ctg Leu	caa Gln	gag Glu 125	acc Thr	tcc Ser	ctg Leu	gct Ala	501
gga Gly 130	gtg Val	gcc Ala	aac Asn	caa Gln	ctg Leu 135	cta Leu	gac Asp	agg Arg	ttt Phe	atc Ile 140	ttt Phe	gaa Glu	gac Asp	cag Gln	atc Ile 145	549
cgg Arg	cct Pro	cag Gln	gac Asp	cga Arg 150	gag Glu	gag Glu	ctg Leu	ctc Leu	cgg Arg 155	gcc Ala	ctg Leu	ctg Leu	ctt Leu	aaa Lys 160	cac His	597
agc Ser	cac His	gct Ala	gga Gly 165	gag Glu	ctg Leu	gag Glu	gcc Ala	ctg Leu 170	ggg Gly	ggt Gly	gtg Val	aag Lys	cct Pro 175	gca Ala	gtc Val	645
ctg Leu	aca Thr	cgc Arg 180	tct Ser	ggg Gly	gat Asp	cct Pro	tca Ser 185	cag Gln	cct Pro	ctg Leu	ctc Leu	ccc Pro 190	caa Gln	cac His	tcc Ser	693
tca Ser	ctg Leu 195	gag Glu	aca Thr	cag Gln	ctc Leu	ttc Phe 200	tgt Cys	gag Glu	cag Gln	gga Gly	gat Asp 205	ggg Gly	ggc Gly	aca Thr	gaa Glu	741
ggg Gly 210	cac His	tca Ser	cca Pro	tct Ser	gga Gly 215	att Ile	ctg Leu	gaa Glu	aag Lys	att Ile 220	ccc Pro	ccg Pro	gat Asp	tca Ser	gag Glu 225	789
gcc Ala	acg Thr	ttg Leu	gtg Val	cta Leu 230	gtg Val	ggc Gly	cgc Arg	gcc Ala	gac Asp 235	ttc Phe	ctg Leu	gag Glu	cag Gln	ccg Pro 240	gtg Val	837
ctg Leu	ggc Gly	ttc Phe	gtg Val 245	agg Arg	ctg Leu	cag Gln	gag Glu	gca Ala 250	gcg Ala	gag Glu	ctg Leu	gag Glu	gcg Ala 255	gtg Val	gag Glu	885
ctg Leu	ccg Pro	gtg Val 260	cct Pro	ata Ile	cgc Arg	ttc Phe	ctc Leu 265	ttt Phe	gtg Val	ttg Leu	ctg Leu	gga Gly 270	cct Pro	gag Glu	gcc Ala	933
ccc Pro	cac His 275	atc Ile	gat Asp	tac Tyr	acc Thr	cag Gln 280	ctt Leu	ggc Gly	cgg Arg	gct Ala	gct Ala 285	gcc Ala	acc Thr	ctc Leu	atg Met	981
tca Ser 290	gag Glu	agg Arg	gtg Val	ttc Phe	cgc Arg 295	ata Ile	gat Asp	gcc Ala	tac Tyr	atg Met 300	gct Ala	cag Gln	agc Ser	cga Arg	ggg Gly 305	1029
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cct Pro	ccc Pro	acc Thr	gat Asp 325	gcc Ala	ccc Pro	tcc Ser	gag Glu	cag Gln 330	gca Ala	ctg Leu	ctc Leu	agt Ser	ctg Leu 335	gtg Val	cct Pro	1125
gtg Val	cag Gln	agg Arg 340	gag Glu	cta Leu	ctt Leu	cga Arg	agg Arg 345	cgc Arg	tat Tyr	cag Gln	tcc Ser	agc Ser 350	cct Pro	gcc Ala	aag Lys	1173
cca Pro	gac Asp	tcc Ser	agc Ser	ttc Phe	tac Tyr	aag Lys	ggc Gly	cta Leu	gac Asp	tta Leu	aat Asn	ggg Gly	ggc Gly	cca Pro	gat Asp	1221

seqlist.txt																
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atc Ile	cgg Arg	cgc Arg	cgc Arg	tac Tyr 390	ccc Pro	tat Tyr	tac Tyr	ctg Leu	agt Ser 395	gac Asp	atc Ile	aca Thr	gat Asp	gca Ala 400	ttc Phe	1317
agc Ser	ccc Pro	cag Gln	gtc Val 405	ctg Leu	gct Ala	gcc Ala	gtc Val	atc Ile 410	ttc Phe	atc Ile	tac Tyr	ttt Phe	gct Ala 415	gca Ala	ctg Leu	1365
tca Ser	ccc Pro	gcc Ala 420	atc Ile	acc Thr	ttc Phe	ggc Gly	ggc Gly 425	ctc Leu	ctg Leu	gga Gly	gaa Glu	aag Lys 430	acc Thr	cgg Arg	aac Asn	1413
cag Gln	atg Met 435	gga Gly	gtg Val	tcg Ser	gag Glu	ctg Leu 440	ctg Leu	atc Ile	tcc Ser	act Thr	gca Ala 445	gtg Val	cag Gln	ggc Gly	att Ile	1461
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aac Asn	ggt Gly	cta Leu	gag Glu 485	tac Tyr	atc Ile	gtg Val	ggc Gly	cgc Arg 490	gtg Val	tgg Trp	atc Ile	ggc Gly	ttc Phe 495	tgg Trp	ctc Leu	1605
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gac Asp	cac His	cca Pro	cta Leu	cag Gln 550	aag Lys	act Thr	tat Tyr	aac Asn	tac Tyr 555	aac Asn	gtg Val	ttg Leu	atg Met	gtg Val 560	ccc Pro	1797
aaa Lys	cct Pro	cag Gln	ggc Gly 565	ccc Pro	ctg Leu	ccc Pro	aac Asn	aca Thr 570	gcc Ala	ctc Leu	ctc Leu	tcc Ser	ctt Leu 575	gtg Val	ctc Leu	1845
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gtc Val 610	ccc Pro	atc Ile	tcc Ser	atc Ile	ctg Leu 615	atc Ile	atg Met	gtc Val	ctg Leu	gtg Val 620	gat Asp	ttc Phe	ttc Phe	att Ile	cag Gln 625	1989
gat Asp	acc Thr	tac Tyr	acc Thr	cag Gln	aaa Lys	ctc Leu	tcg Ser	gtg Val	cct Pro	gat Asp	ggc Gly	ttc Phe	aag Lys	gtg Val	tcc Ser	2037

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gag	ttt	ccc	atc	tgg	atg	atg	ttt	gcc	tcc	gcc	ctg	cct	gct	ctg	ctg	2133
Glu	Phe	Pro	Ile	Trp	Met	Met	Phe	Ala	Ser	Ala	Leu	Pro	Ala	Leu	Leu	
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gtc	ttc	atc	ctc	ata	ttc	ctg	gag	tct	cag	atc	acc	acg	ctg	att	gtc	2181
Val	Phe	Ile	Leu	Ile	Phe	Leu	Glu	Ser	Gln	Ile	Thr	Thr	Leu	Ile	Val	
			675				680						685			
agc	aaa	cct	gag	cgc	aag	atg	gtc	aag	ggc	tcc	ggc	ttc	cac	ctg	gac	2229
Ser	Lys	Pro	Glu	Arg	Lys	Met	Val	Lys	Gly	Ser	Gly	Phe	His	Leu	Asp	
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ctg	ctg	ctg	gta	gta	ggc	atg	ggg	gtg	gtg	gcc	gcc	ctc	ttt	ggg	atg	2277
Leu	Leu	Leu	Val	Val	Gly	Met	Gly	Gly	Val	Ala	Ala	Leu	Phe	Gly	Met	
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ccc	tgg	ctc	agt	gcc	acc	acc	gtg	cgt	tcc	gtc	acc	cat	gcc	aac	gcc	2325
Pro	Trp	Leu	Ser	Ala	Thr	Thr	Val	Arg	Ser	Val	Thr	His	Ala	Asn	Ala	
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Leu	Thr	Val	Met	Gly	Lys	Ala	Ser	Thr	Pro	Gly	Ala	Ala	Ala	Gln	Ile	
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cag	gag	gtc	aaa	gag	cag	cgg	atc	agt	gga	ctc	ctg	gtc	gct	gtg	ctt	2421
Gln	Glu	Val	Lys	Glu	Gln	Arg	Ile	Ser	Gly	Leu	Leu	Val	Ala	Val	Leu	
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gtg	ggc	ctg	tcc	atc	ctc	atg	gag	ccc	atc	ctg	tcc	cgc	atc	ccc	ctg	2469
Val	Gly	Leu	Ser	Ile	Leu	Met	Glu	Pro	Ile	Leu	Ser	Arg	Ile	Pro	Leu	
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gct	gta	ctg	ttt	ggc	atc	ttc	ctc	tac	atg	ggg	gtc	acg	tcg	ctc	agc	2517
Ala	Val	Leu	Phe	Gly	Ile	Phe	Leu	Tyr	Met	Gly	Val	Thr	Ser	Leu	Ser	
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ggc	atc	cag	ctc	ttt	gac	cgc	atc	ttg	ctt	ctg	ttc	aag	cca	ccc	aag	2565
Gly	Ile	Gln	Leu	Phe	Asp	Arg	Ile	Leu	Leu	Leu	Phe	Lys	Pro	Pro	Lys	
			805				810						815			
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Tyr	His	Pro	Asp	Val	Pro	Tyr	Val	Lys	Arg	Val	Lys	Thr	Trp	Arg	Met	
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cac	tta	ttc	acg	ggc	atc	cag	atc	atc	tgc	ctg	gca	gtg	ctg	tgg	gtg	2661
His	Leu	Phe	Thr	Gly	Ile	Gln	Ile	Ile	Cys	Leu	Ala	Val	Leu	Trp	Val	
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gtg	aag	tcc	acg	ccg	gcc	tcc	ctg	gcc	ctg	ccc	ttc	gtc	ctc	atc	ctc	2709
Val	Lys	Ser	Thr	Pro	Ala	Ser	Leu	Ala	Leu	Pro	Phe	Val	Leu	Ile	Leu	
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Thr	Val	Pro	Leu	Arg	Arg	Val	Leu	Leu	Pro	Leu	Ile	Phe	Arg	Asn	Val	
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seq1ist.txt

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 Gly Asp Val Arg Ala Phe Leu Arg Glu His Pro Ser Leu Arg Leu Gln
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acg gac gcc cgc aag gtg agg tgc atc ctg aca ggt cac gag ctg ccc 152
 Thr Asp Ala Arg Lys Val Arg Cys Ile Leu Thr Gly His Glu Leu Pro
25 30 35

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 Cys Arg Leu Pro Glu Leu Gln Val Tyr Thr Arg Gly Lys Lys Tyr Gln
40 45 50

cgg ctg gtc cgc gcc tcc ccg gcc ttc gac tat gca gag ttc gag ccg 248
 Arg Leu Val Arg Ala Ser Pro Ala Phe Asp Tyr Ala Glu Phe Glu Pro
55 60 65

cac atc gtg ccc agc acc aag aac ccg cac cag ttg ttc tgc aaa ctc 296
 His Ile Val Pro Ser Thr Lys Asn Pro His Gln Leu Phe Cys Lys Leu
70 75 80 85

acc ctg cgg cac atc aac aag tgc cca gaa cac gtg ctg agg cac acc 344
 Thr Leu Arg His Ile Asn Lys Cys Pro Glu His Val Leu Arg His Thr
90 95 100

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 Gln Gly Arg Arg Tyr Gln Arg Ala Leu Cys Lys Tyr Glu Glu Cys Gln
105 110 115

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 Lys Gln Gly Val Glu Tyr Val Pro Ala Cys Leu Val His Arg Arg Arg
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 Arg Arg Glu Asp Gln Met Asp Gly Asp Gly Pro Arg Pro Arg Glu Ala
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seq1ist.txt

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Ser Met Thr Asp Leu Tyr Pro Pro Glu Leu Phe Thr Arg Lys Asp Leu	
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Gly Ser Thr Glu Asp Gly Asp Gly Thr Asp Asp Phe Leu Thr Asp Lys	
185 190 195	
gag gat gag aag gca aag ccc cca aga gag aag gcc act gat gag ggc	680
Glu Asp Glu Lys Ala Lys Pro Pro Arg Glu Lys Ala Thr Asp Glu Gly	
200 205 210	
agg aga gag acg acc gtg tac cga ggg ctg gtc cag aag cgc ggg aag	728
Arg Arg Glu Thr Thr Val Tyr Arg Gly Leu Val Gln Lys Arg Gly Lys	
215 220 225	
aag cag ttg ggc tcg ttg aaa aag aag ttc aag agt cat cac cgc aaa	776
Lys Gln Leu Gly Ser Leu Lys Lys Lys Phe Lys Ser His His Arg Lys	
230 235 240 245	
ccc aag agc ttc agc tcc tgt aaa cag cca ggt taa taaaagcaca	822
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Cys Gln Trp Leu Pro Ile Leu Ile Leu Leu Gly Thr Gly His Gly	
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Pro Gly Val Glu Gly Val Thr His Tyr Lys Ala Gly Asp Pro Val Ile	
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Leu Tyr Val Asn Lys Val Gly Pro Tyr His Asn Pro Gln Glu Thr Tyr	
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cac tac tat cag ctt cca gtc tgc tgc cct gag aag ata cgt cac aaa	242
His Tyr Tyr Gln Leu Pro Val Cys Cys Pro Glu Lys Ile Arg His Lys	
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Ser Leu Ser Leu Gly Glu Val Leu Asp Gly Asp Arg Met Ala Glu Ser	
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Leu Tyr Glu Ile Arg Phe Arg Glu Asn Val Glu Lys Arg Ile Leu Cys	

seq1ist.txt																
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gaa Glu	gaa Glu 125	ctg Leu	tac Tyr	tac Tyr	ttt Phe	gaa Glu 130	ttt Phe	gtg Val	gta Val	gat Asp	gac Asp 135	ttg Leu	cca Pro	atc Ile	cgg Arg	434
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Gly	Lys	Leu	Leu	Ser	Val	Glu	Thr	Pro	Arg	Ala	Leu	His	His	Tyr	Arg	
			1050					1055					1060			
ggc	cgc	tac	acc	gtg	gag	gac	atc	cag	cgc	ctg	gtg	ccc	gac	agc	gac	3570
Gly	Arg	Tyr	Thr	Val	Glu	Asp	Ile	Gln	Arg	Leu	Val	Pro	Asp	Ser	Asp	
		1065					1070					1075				
gtg	gag	gag	ctg	ctg	cag	atc	ctc	gat	gcc	atg	gac	atc	tgc	gcc	cgg	3618
Val	Glu	Glu	Leu	Leu	Gln	Ile	Leu	Asp	Ala	Met	Asp	Ile	Cys	Ala	Arg	
	1080					1085					1090					
gac	ctg	agc	agc	ggg	acc	atg	gtg	gac	gtc	cca	gcc	ctg	atc	aag	aca	3666
Asp	Leu	Ser	Ser	Gly	Thr	Met	Val	Asp	Val	Pro	Ala	Leu	Ile	Lys	Thr	
1095					1100					1105					1110	
gac	aac	ctg	cac	cgc	tcc	tgg	gct	gat	gag	gag	gac	gag	gtg	atg	gtg	3714
Asp	Asn	Leu	His	Arg	Ser	Trp	Ala	Asp	Glu	Glu	Asp	Glu	Val	Met	Val	
				1115					1120					1125		
tat	ggt	ggc	gtg	cgc	atc	gtg	ccc	gtg	gaa	cac	ctc	acc	ccc	ttc	cca	3762
Tyr	Gly	Gly	Val	Arg	Ile	Val	Pro	Val	Glu	His	Leu	Thr	Pro	Phe	Pro	
			1130					1135					1140			
tgt	ggc	atc	ttt	cac	aag	gtc	cag	gtg	aac	ctg	tgc	cgg	tgg	atc	cac	3810
Cys	Gly	Ile	Phe	His	Lys	Val	Gln	Val	Asn	Leu	Cys	Arg	Trp	Ile	His	
		1145					1150					1155				
cag	caa	agc	aca	gag	ggc	gac	gcg	gac	atc	cgc	ctg	tgg	gtg	aat	ggc	3858
Gln	Gln	Ser	Thr	Glu	Gly	Asp	Ala	Asp	Ile	Arg	Leu	Trp	Val	Asn	Gly	
	1160					1165					1170					
tgc	aag	ctg	gcc	aac	cgt	ggg	gcc	gag	ctg	ctg	gtg	ctg	ctg	gtc	aac	3906
Cys	Lys	Leu	Ala	Asn	Arg	Gly	Ala	Glu	Leu	Leu	Val	Leu	Leu	Val	Asn	
1175					1180				1185						1190	
cac	ggc	cag	ggc	att	gag	gtc	cag	gtc	cgt	ggc	ctg	gag	acg	gag	aag	3954
His	Gly	Gln	Gly	Ile	Glu	Val	Gln	Val	Arg	Gly	Leu	Glu	Thr	Glu	Lys	
				1195					1200					1205		
atc	aag	tgc	tgc	ctg	ctg	ctg	gac	tcg	gtg	tgc	agc	acc	att	gag	aac	4002
Ile	Lys	Cys	Cys	Leu	Leu	Leu	Asp	Ser	Val	Cys	Ser	Thr	Ile	Glu	Asn	
			1210					1215					1220			
gtc	atg	gcc	acc	acg	ctg	cca	ggg	ctc	ctg	acc	gtg	aag	cat	tac	ctg	4050
Val	Met	Ala	Thr	Thr	Leu	Pro	Gly	Leu	Leu	Thr	Val	Lys	His	Tyr	Leu	
		1225					1230					1235				
agc	ccc	cag	cag	ctg	cgg	gag	cac	cat	gag	ccc	gtc	atg	atc	tac	cag	4098
Ser	Pro	Gln	Gln	Leu	Arg	Glu	His	His	Glu	Pro	Val	Met	Ile	Tyr	Gln	
	1240					1245					1250					
cca	cgg	gac	ttc	ttc	cgg	gca	cag	act	ctg	aag	gaa	acc	tca	ctg	acc	4146
Pro	Arg	Asp	Phe	Phe	Arg	Ala	Gln	Thr	Leu	Lys	Glu	Thr	Ser	Leu	Thr	
1255					1260					1265					1270	
aac	acc	atg	ggg	ggg	tac	aag	gaa	agc	ttc	agc	agc	atc	atg	tgc	ttc	4194
Asn	Thr	Met	Gly	Gly	Tyr	Lys	Glu	Ser	Phe	Ser	Ser	Ile	Met	Cys	Phe	
				1275					1280					1285		

seq1ist.txt

ggg tgt cac gac gtc tac tca cag gcc agc ctc ggc atg gac atc cat 4242
 Gly Cys His Asp Val Tyr Ser Gln Ala Ser Leu Gly Met Asp Ile His
 1290 1295 1300
 gca tca gac ctg aac ctc ctc act cgg agg aaa ctg agt cgc ctg ctg 4290
 Ala Ser Asp Leu Asn Leu Leu Thr Arg Arg Lys Leu Ser Arg Leu Leu
 1305 1310 1315
 gac ccg ccc gac ccc ctg ggg aag gac tgg tgc ctt ctc gcc atg aac 4338
 Asp Pro Pro Asp Pro Leu Gly Lys Asp Trp Cys Leu Leu Ala Met Asn
 1320 1325 1330
 tta ggc ctc cct gac ctc gtg gca aag tac aac acc aat aac ggg gct 4386
 Leu Gly Leu Pro Asp Leu Val Ala Lys Tyr Asn Thr Asn Asn Gly Ala
 1335 1340 1345 1350
 ccc aag gat ttc ctc ccc agc ccc ctc cac gcc ctg ctg cgg gaa tgg 4434
 Pro Lys Asp Phe Leu Pro Ser Pro Leu His Ala Leu Leu Arg Glu Trp
 1355 1360 1365
 acc acc tac cct gag agc aca gtg ggc acc ctc atg tcc aaa ctg agg 4482
 Thr Thr Tyr Pro Glu Ser Thr Val Gly Thr Leu Met Ser Lys Leu Arg
 1370 1375 1380
 gag ctg ggt cgc cgg gat gcc gca gac ctt ttg ctg aag gca tcc tct 4530
 Glu Leu Gly Arg Arg Asp Ala Ala Asp Leu Leu Leu Lys Ala Ser Ser
 1385 1390 1395
 gtg ttc aaa atc aac ctg gat ggc aat ggc cag gag gcc tat gcc tcg 4578
 Val Phe Lys Ile Asn Leu Asp Gly Asn Gly Gln Glu Ala Tyr Ala Ser
 1400 1405 1410
 agc tgc aac agc ggc acc tct tac aat tcc att agc tct gtt gta tcc 4626
 Ser Cys Asn Ser Gly Thr Ser Tyr Asn Ser Ile Ser Ser Val Val Ser
 1415 1420 1425 1430
 cgg tga gggcagcctc tggcttggac agggctctgtt tggactgcag aaccaagggg 4682
 Arg *

gtgatgtagc ccattccttcc ctttggagat gctgaggggtg tttcttcctg caccacagc 4742
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 ccagtacctt gcttcttact gataattttg ctggaattcc taacttttca atgacatttt 4982
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 aggagaaact cccatgtatg gaatcccact gtatgattta taaacagaca atatgtgagt 5162
 gccttttgca gaagagggtg tgtttgaaat catcggagtc agccaggagc tgtcaccaag 5222
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 catagcagat ggtttccaca tttagatcct ggtttcataa cttcctgtac ttgaagtcta 5642
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 aattgatagg agggaacatg tcctaattct tctgtcctga gaagcatgta atgttaattgt 5762
 tatatcatat gtatatatat atatgcacta tgtatatata tatatatata tactgggtatt 5822
 tttacttaat ctataaaatg tcgttaaaaaa gttgtttgtt tttttctttt ttataaata 5882
 aactgttgct cgtaaaaaa aaaaaaaa 5910

<210> 12
 <211> 1579
 <212> DNA
 <213> Homo sapiens

seq1ist.txt

<220>

<221> CDS

<222> (313)...(867)

<223> Human RAP1A, member of RAS oncogene family (RAP1A)
mRNA coding region

<400> 12

```

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ctgccgggttc gaacacacgc gagaagagca aagaagttaa aagagaagtg tctgtgtggc 120
tccttccacg tgggtgaagg actgtgccag ctgagagggtg gtagagcagg aagctgcctg 180
agacctccat ttatttggtg aaaaaccgcc gcccttaaga gagcaagtcg agggccgtgt 240
aggagttgga ggagagaaat gaaattttgg aagagtcagc agaagatcgt cagtatttaa 300
acacatcaca tc atg cgt gag tac aag cta gtg gtc ctt ggt tca gga ggc 351
                Met Arg Glu Tyr Lys Leu Val Val Leu Gly Ser Gly Gly
                        1                      5                      10

```

```

gtt ggg aag tct gct ctg aca gtt cag ttt gtt cag gga att ttt gtt 399
Val Gly Lys Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val
                15                      20                      25

```

```

gaa aaa tat gac cca acg ata gaa gat tcc tac aga aag caa gtt gaa 447
Glu Lys Tyr Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Glu
30                      35                      40                      45

```

```

gtc gat tgc caa cag tgt atg ctc gaa atc ctg gat act gca ggg aca 495
Val Asp Cys Gln Gln Cys Met Leu Glu Ile Leu Asp Thr Ala Gly Thr
                50                      55                      60

```

```

gag caa ttt aca gca atg agg gat ttg tat atg aag aac ggc caa ggt 543
Glu Gln Phe Thr Ala Met Arg Asp Leu Tyr Met Lys Asn Gly Gln Gly
                65                      70                      75

```

```

ttt gca cta gta tat tct att aca gct cag tcc acg ttt aac gac tta 591
Phe Ala Leu Val Tyr Ser Ile Thr Ala Gln Ser Thr Phe Asn Asp Leu
                80                      85                      90

```

```

cag gac ctg agg gaa cag att tta cgg gtt aag gac acg gaa gat gtt 639
Gln Asp Leu Arg Glu Gln Ile Leu Arg Val Lys Asp Thr Glu Asp Val
                95                      100                      105

```

```

cca atg att ttg gtt ggc aat aaa tgt gac ctg gaa gat gag cga gta 687
Pro Met Ile Leu Val Gly Asn Lys Cys Asp Leu Glu Asp Glu Arg Val
110                      115                      120                      125

```

```

gtt ggc aaa gag cag ggc cag aat tta gca aga cag tgg tgt aac tgt 735
Val Gly Lys Glu Gln Gly Gln Asn Leu Ala Arg Gln Trp Cys Asn Cys
                130                      135                      140

```

```

gcc ttt tta gaa tct tct gca aag tca aag atc aat gtt aat gag ata 783
Ala Phe Leu Glu Ser Ser Ala Lys Ser Lys Ile Asn Val Asn Glu Ile
                145                      150                      155

```

```

ttt tat gac ctg gtc aga cag ata aat agg aaa aca cca gtg gaa aag 831
Phe Tyr Asp Leu Val Arg Gln Ile Asn Arg Lys Thr Pro Val Glu Lys
                160                      165                      170

```

```

aag aag cct aaa aag aaa tca tgt ctg ctg ctc tag gcccatagtc 877
Lys Lys Pro Lys Lys Lys Ser Cys Leu Leu Leu *
                175                      180

```

```

agcagcagct ctgagccaga ttacaggaat gaagaactgt tgcctaattg gaaagtgcca 937
gcattccaga ctcaaaaaat aaaaaatctg aagaggcttc tcctgtttta tatattatgt 997
gaagaattta gatcttataat tggtttgcac aagttccctg gagaaaaaaa ttgctctgtg 1057
tatatctctt ggaaaataag acaatagtat ttctcctttg caatagcagt tataacagat 1117
gtgaaaatat acttgactct aatatgatta tacaaaagag catggatgca tttcaaatgt 1177
tagatatgtc tactataatc aaatgatttc atattgatct ttttatcatg atcctaccta 1237
tcaagcacta aaaagttgaa ccattatact ttatatctgt aatgatactg attatgaaat 1297
gtcccctgaa actcattgca gcagataact tttttgagtc attgacttca ttttatattt 1357

```

seq1ist.txt

```

aaaaaattat ggaatatcat ctgtcattat attctaatta aaattgtgca taatgctttg 1417
gaaaaatggg tcttttatag gaaaaaaact gggataactg atttctatgg ctttcaaagc 1477
taaaatatat aatatactaa accaactcta atattgcttc ttgtgtttta ctgtcagatt 1537
aaattacagc ttttatggat gattaaattt tagtacattt tc 1579

```

```

<210> 13
<211> 3222
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (0)...(0)
<223> Human down-regulator of transcription 1,
      TBP-binding (negative cofactor 2) (DR1) mRNA
      coding region

```

```

<400> 13
gagcggcttc ctgcaaacct tccctggcat ctggaggggac caccgttgcc gcgtcttcgg 60
cttccacgat ctgcgttcgg gctacgcggc cacggcggca gccactgcga ctcccactgt 120
gcctggctct gtccatatta gttcccaggc ggccgtcgcc gttccagcag cggcagcggc 180
agcggcagcg gcggacatgt tgtgaggcgg cggcgcgggg gtctgaagga tggtttggcc 240
gaggcggcgg caacggctgc tggcggcggc ggagcgggca gcggggcctc gggctctata 300
gagcggagcc cgctgggtac ccgcccggta ccgcggcgag gccagtgtccc ctggatcttg 360
cctctgtctc gacgccgttg gggaccagt ggcgacagc gcccgcccct ctgaggagac 420
acgaaggtgg ttccccagcc gctcaaat tccgaccacc gcgctttccc ctctcagcc 480
tggtgtgtgc tctctctaga atcctcgggc cccactttc ttcccaaact catcctaaat 540
ctctcacaca cgcgagtgtt cccagccctc aagccagctg ctctccgtt cattttctgc 600
accctcttcg caaagcacc cccgggatca ctctccgagg gcgacttttt gagaaatctc 660
ggtggagtag tggaccagag ctggggagtt tttaaaagcc ggggcgcgag aaacaggaag 720
gtactatggc ttctctgtct ggcaacgat atgatctcac tatccccaga gctgctatca 780
ataaaatgat caaagagact cttcctaatt tccgggtggc caacgatgct cgagagctgg 840
tggtgaactg ctgcactgaa ttcatcacc atctcaccag agcatgtcat acaagcacta gaaagtgttg 960
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gttctcttgg tttaactgag gtttatgaat attcaaacct ttgctggggg aaagaaatga 2160
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atgttgatga gatagaagaa attgtttttt aaaaagttaa agtaccaaag gtagtctagt 2940
ctagaacgat aagttaatac gtgttggtct ttctaatttg tactgtaaca tccttatact 3000

```

seq1ist.txt

```

ttctatttta agtataatctg tttcttaagt aaacaactta gatattttcc acaccttttt 3060
ttttttttct gatgcagagt tcagggttaat attttactgc atctgataat gtattatacg 3120
tttgaagcct agtgactttt cattttgaca ttcttgtgat ttcatatgct gtattcttca 3180
agcaataaaa ttgtgatgtg ttttataaaa aaaaaaaaaa aa 3222

```

<210> 14
 <211> 3541
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (76)...(3504)
 <223> Human Janus kinase 1 (JAK1) mRNA coding region

```

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gaggactgca atgcc atg gct ttc tgt gct aaa atg agg agc tcc aag aag 111
          Met Ala Phe Cys Ala Lys Met Arg Ser Ser Lys Lys
          1          5          10

act gag gtg aac ctg gag gcc cct gag cca ggg gtg gaa gtg atc ttc 159
Thr Glu Val Asn Leu Glu Ala Pro Glu Pro Gly Val Glu Val Ile Phe
          15          20          25

tat ctg tcg gac agg gag ccc ctc cgg ctg ggc agt gga gag tac aca 207
Tyr Leu Ser Asp Arg Glu Pro Leu Arg Leu Gly Ser Gly Glu Tyr Thr
          30          35          40

gca gag gaa ctg tgc atc agg gct gca cag gca tgc cgt atc tct cct 255
Ala Glu Glu Leu Cys Ile Arg Ala Ala Gln Ala Cys Arg Ile Ser Pro
          45          50          55          60

ctt tgt cac aac ctc ttt gcc ctg tat gac gag aac acc aag ctc tgg 303
Leu Cys His Asn Leu Phe Ala Leu Tyr Asp Glu Asn Thr Lys Leu Trp
          65          70          75

tat gct cca aat cgc acc atc acc gtt gat gac aag atg tcc ctc cgg 351
Tyr Ala Pro Asn Arg Thr Ile Thr Val Asp Asp Lys Met Ser Leu Arg
          80          85          90

ctc cac tac cgg atg agg ttc tat ttc acc aat tgg cat gga acc aac 399
Leu His Tyr Arg Met Arg Phe Tyr Phe Thr Asn Trp His Gly Thr Asn
          95          100          105

gac aat gag cag tca gtg tgg cgt cat tct cca aag aag cag aaa aat 447
Asp Asn Glu Gln Ser Val Trp Arg His Ser Pro Lys Lys Gln Lys Asn
          110          115          120

ggc tac gag aaa aaa aag att cca gat gca acc cct ctc ctt gat gcc 495
Gly Tyr Glu Lys Lys Lys Ile Pro Asp Ala Thr Pro Leu Leu Asp Ala
          125          130          135          140

agc tca ctg gag tat ctg ttt gct cag gga cag tat gat ttg gtg aaa 543
Ser Ser Leu Glu Tyr Leu Phe Ala Gln Gly Gln Tyr Asp Leu Val Lys
          145          150          155

tgc ctg gct cct att cga gac ccc aag acc gag cag gat gga cat gat 591
Cys Leu Ala Pro Ile Arg Asp Pro Lys Thr Glu Gln Asp Gly His Asp
          160          165          170

att gag aac gag tgt cta ggg atg gct gtc ctg gcc atc tca cac tat 639
Ile Glu Asn Glu Cys Leu Gly Met Ala Val Leu Ala Ile Ser His Tyr
          175          180          185

gcc atg atg aag aag atg cag ttg cca gaa ctg ccc aag gac atc agc 687
Ala Met Met Lys Lys Met Gln Leu Pro Glu Leu Pro Lys Asp Ile Ser
          190          195          200

```

seq1ist.txt

tac Tyr 205	aag Lys	cga Arg	tat Tyr	att Ile	cca Pro 210	gaa Glu	aca Thr	ttg Leu	aat Asn	aag Lys 215	tcc Ser	atc Ile	aga Arg	cag Gln	agg Arg 220	735
aac Asn	ctt Leu	ctc Leu	acc Thr	agg Arg 225	atg Met	cgg Arg	ata Ile	aat Asn	aat Asn 230	gtt Val	ttc Phe	aag Lys	gat Asp	ttc Phe 235	cta Leu	783
aag Lys	gaa Glu	ttt Phe	aac Asn 240	aac Asn	aag Lys	acc Thr	att Ile	tgt Cys 245	gac Asp	agc Ser	agc Ser	gtg Val	tcc Ser 250	acg Thr	cat His	831
gac Asp	ctg Leu	aag Lys 255	gtg Val	aaa Lys	tac Tyr	ttg Leu	gct Ala 260	acc Thr	ttg Leu	gaa Glu	act Thr	ttg Leu 265	aca Thr	aaa Lys	cat His	879
tac Tyr	ggt Gly 270	gct Ala	gaa Glu	ata Ile	ttt Phe	gag Glu 275	act Thr	tcc Ser	atg Met	tta Leu	ctg Leu 280	att Ile	tca Ser	tca Ser	gaa Glu	927
aat Asn 285	gag Glu	atg Met	aat Asn	tgg Trp	ttt Phe 290	cat His	tcg Ser	aat Asn	gac Asp	ggt Gly 295	gga Gly	aac Asn	gtt Val	ctc Leu	tac Tyr 300	975
tac Tyr	gaa Glu	gtg Val	atg Met	gtg Val 305	act Thr	ggg Gly	aat Asn	ctt Leu	gga Gly 310	atc Ile	cag Gln	tgg Trp	agg Arg	cat His 315	aaa Lys	1023
cca Pro	aat Asn	gtt Val	gtt Val 320	tct Ser	gtt Val	gaa Glu	aag Lys	gaa Glu 325	aaa Lys	aat Asn	aaa Lys	ctg Leu	aag Lys 330	cgg Arg	aaa Lys	1071
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gaa Glu	gag Glu 350	tgg Trp	aac Asn	aat Asn	ttt Phe	tca Ser 355	ttc Phe	ttc Phe	cct Pro	gaa Glu	atc Ile 360	act Thr	cac His	att Ile	gta Val	1167
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seqlist.txt

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cac His 990	cgg Arg	gac Asp	ttg Leu	gca Ala	gca Ala	aga Arg	aat Asn 995	gtc Val	ctt Leu	gtt Val	gag Glu 1000	agt Ser	gaa Glu	cac His	caa Gln	3087
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seqlist.txt

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Val	Asp	Tyr	Gly	Lys	Lys	Ser	Lys	Leu	Glu	Phe	Ser	Ile	Tyr	Pro	Ala	
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Pro	Gln	Val	Ser	Thr	Ala	Val	Val	Glu	Pro	Tyr	Asn	Ser	Ile	Leu	Thr	
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Tyr	Arg	Gly	Asp	Val	Val	Pro	Lys	Asp	Val	Asn	Ala	Ala	Ile	Ala	Thr	
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Tyr Ala Lys Arg Ala Phe Val 405 His Trp Tyr Val Gly 410 Glu Gly Met Glu	
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 Met Thr Glu Pro Gly Ala Ser Pro Glu Asp Pro Trp Val Lys Val
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 Asp Tyr His Gln Glu Ala Tyr Lys Glu Ser Tyr Lys Asp Arg Arg Arg
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 Glu Glu Val Ser Thr Leu Arg Lys Asp Val Thr Ala Leu Lys Ile Met
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 Lys Val Asn Tyr Glu Gln Ile Val Lys Ala His Gln Asp Asn Pro His
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seq1ist.txt

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His Cys Lys Pro Gln Thr Leu Arg Glu Ile Val Ile Gly Val Leu His
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Gln Leu Lys Asn Gln Leu Tyr *
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Ala Gly Thr Tyr Gly Asp Val Tyr Lys Ala Arg Asp Thr Val Thr Ser
25 30 35

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